In the claims:

1. (**Currently amended**) A method of assigning a sample to a known class, comprising the steps of:

   a. determining a weighted vote for one or more informative genes for the known class in said sample in accordance with a model built with a weighted voting scheme, wherein the magnitude of each vote depends on the expression level of the one or more informative genes in said sample and on the degree of correlation of the one or more informative genes' expression with class distinction; ~~and~~

   b. summing the votes to determine a winning class and a prediction strength[[,]];

   c. assigning said sample to the winning class, which winning class is a known class, if the prediction strength is greater than a prediction strength threshold; and

   d. providing an output indicating assignment of said sample to the winning class, ~~wherein said sample is assigned to the winning class if the prediction strength is greater than a prediction strength threshold, and~~ wherein the known class is a cancer disease class selected from any of Acute Lymphoblastic Leukemia (ALL), Acute Myeloid Leukemia (AML), glioblastoma, medulloblastoma, folicular lymphoma, or diffuse large B cell lymphoma.

2. (**Previously presented**) The method of Claim 1, wherein the prediction strength is determined by:

$$(V_{win} - V_{lose}) / (V_{win} + V_{lose}),$$

wherein V_{win} and V_{lose} are the vote totals for one or more winning and losing classes, respectively.

3. (**Original**) The method of Claim 2, wherein the number of informative genes used in the weighted voting scheme is at least 50.

4. (**Previously presented**) The method of Claim 1, wherein the cancer disease class is Acute Lymphoblastic Leukemia (ALL) or Acute Myeloid Leukemia (AML).

5. **(Previously presented)** The method of Claim 2, wherein the cancer disease class is Acute Lymphoblastic Leukemia (ALL) or Acute Myeloid Leukemia (AML).

6. **(Previously presented)** The method of Claim 3, wherein the cancer disease class is Acute Lymphoblastic Leukemia (ALL) or Acute Myeloid Leukemia (AML).

7. **(Previously presented)** The method of Claim 6, wherein the informative genes encode proteins selected from the group consisting of: c-myb, MB-1, cyclinD3, Rb Ap48, SNF2, E2A, topoisomerase II β, TFIIEβ, MCM3, Op 18, zyxin, HoxA9, CD33, and CD11c.

8. **(Cancelled)**

9. **(Currently amended)** A method of determining a weighted vote for an informative gene to be used in classifying a sample to be tested, comprising:

   a. determining a weighted vote for a known class for one or more informative genes in said sample, wherein the magnitude of each vote depends on the expression level of the one or more informative genes in said sample and on the degree of correlation of the one or more informative genes' expression with class distinction; ~~and~~

   b. summing the votes to determine the weighted vote for the known class[[,]]; and

   c. providing an output indicating the weighted vote for the known class,

   wherein the known class is a cancer disease class selected from any of Acute Lymphoblastic Leukemia (ALL), Acute Myeloid Leukemia (AML), glioblastoma, medulloblastoma, folicular lymphoma, or diffuse large B cell lymphoma.

10. **(Previously presented)** The method of Claim 9, wherein the weighted vote is determined according to:

$$V_g = a_g(x_g - b_g),$$

wherein V_g is the weighted vote of the gene, g; a_g is the correlation between gene expression values and class distinction; $b_g = (\mu_1(g) + \mu_2(g)) / 2$ which is the average of the mean $\log_{10}$ expression value in a first class and a second class; x_g is the $\log_{10}$ gene

expression value in the sample to be tested; and wherein a positive V value indicates a vote for the first class, and a negative V value indicates a vote for the second class.

11. **(Original)** The method of Claim 10, wherein the vote for the first class is determined by obtaining a sum of the absolute values of the positive votes for the first class, and the vote for the second class is determined by obtaining a sum of the absolute values of the negative votes for the second class.

12. **(Previously presented)** The method of Claim 11, wherein the weighted vote is determined by a portion of genes that are relevant for determining the classes.

13. **(Original)** The method of Claim 12, wherein a signal to noise routine, a Pearson correlation routine, or a Euclidean distance routine determines the relevant genes.

14. **(Previously presented)** The method of Claim 13, wherein the signal to noise routine is:

$$P(g,c) = ((\mu_1(g) - \mu_2(g)) - ((\sigma_1(g) + \sigma_2(g)),$$

wherein g is the gene expression value; c is the class distinction, $\mu_1(g)$ is the mean of the expression levels for g for the first class; $\mu_2(g)$ is the mean of the expression levels for g for the second class; $\sigma_1(g)$ is the standard deviation for the first class; and $\sigma_2(g)$ is the standard deviation for the second class.

15-64. **(Cancelled)**

65. **(Previously presented)** The method of Claim 3, wherein the cancer disease class is glioblastoma or medulloblastoma.

66. **(Previously presented)** The method of Claim 3, wherein the cancer disease class is folicular lymphoma or diffuse large B cell lymphoma.

67-71. **(Cancelled)**

72. **(Previously presented)** The method of claim 6, wherein the informative genes are markers of hematopoietic lineage.

73. **(New)** The method of claim 1, wherein the output comprises an output assembly.

74. **(New)** The method of claim 9, wherein the output comprises an output assembly.

75. **(New)** The method of claim 73, wherein the output assembly comprises a graphical representation.

76. **(New)** The method of claim 74, wherein the output assembly comprises a graphical representation.